

FIGURE 1

CAGAGAAAACCTCCTCCAAAAGCAGCTCTCACTATCAGAAAACCCAACTAC
AGTTGTGAACGCCTTCATTTTCTGCCTGAGGTCTCAGTCCGTGCGGCCAG
ACTGAAGTGCAGTGGCACAATCATAGCTCGCTGCAGCCTCGACCTTCCAG
GCTTAAACGATTCTCCACCTCAGCCTCTCGAGTTGCTGGGACCACAGGT
CACTGTGCATGGCATCATCCTGGCCCCCTCTAGAGCTCCAATCCTCCAAC
CAGAGCCAGCTCTTCCCTCAAATGCTACGGCCTGTGACAATGCTCCAGA
AGCCTGGGACCTGCTGCACAGAGTGCTGCCGACATTTATCATCTCCATCT
GTTTCTTCGGCCTCCTAGGGAACCTTTTTGTCTGTTGGTCTTCCTCCTG
CCCCGGCGGCAACTGAACGTGGCAGAAATCTACCTGGCCAACCTGGCAGC
CTCTGATCTGGTGTGTTGTCTTGGGCTTGCCCTTCTGGGCAGAGAATATCT
GGAACCAGTTTAACTGGCCTTTCGGAGCCCTCCTCTGCCGTGTCATCAAC
GGGGTCATCAAGGCCAATTTGTTTCATCAGCATCTTCCTGGTGGTGGCCAT
CAGCCAGGACCGCTACCGCGTGCTGGTGCACCCTATGGCCAGCGGAAGGC
AGCAGCGGCGGAGGCAGGCCCCGGGTACCTGCGTGCTCATCTGGGTTGTG
GGGGGCTCTTGAGCATCCCCACATTCTGCTGCGATCCATCCAAGCCGT
CCCAGATCTGAACATCACCGCCTGCATCCTGCTCCTCCCCCATGAGGCCT
GGCACTTTGCAAGGATTGTGGAGTTAAATATTCTGGGTTTCCTCCTACCA
CTGGCTGCGATCGTCTTCTTCAACTACCACATCCTGGCCTCCCTGCGAAC
GCGGGAGGAGGTCAGCAGGACAAGGTGCGGGGGCCGCAAGGATAGCAAGA
CCACAGCGCTGATCCTCACGCTCGTGGTTGCCTTCCTGGTCTGCTGGGCC
CCTTACCACTTCTTTGCCTTCCTGGAATTCTTATTCCAGGTGCAAGCAGT
CCGAGGCTGCTTTTGGGAGGACTTCATTGACCTGGGCCTGCAATTGGCCA
ACTTCTTTGCCTTCACTAACAGCTCCCTGAATCCAGTAATTTATGTCTTT
GTGGGCCCGCTCTTCAGGACCAAGGTCTGGGAACCTTTATAAACAATGCAC
CCCTAAAAGTCTTGCTCCAATATCTTCATCCCATAGGAAAGAAATCTTCC
AACTTTTCTGGCGGAATTAAAACAGCATTGAACCAAGAAAAAAAAAAAAA
AAAAAA SEQ.ID.NO.:1.

FIGURE 2

MET Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln
Ser Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro
Glu Ala Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile
Ser Ile Cys Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu
Val Phe Leu Leu Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr
Leu Ala Asn Leu Ala Ala Ser Asp Leu Val Phe Val Leu Gly Leu
Pro Phe Trp Ala Glu Asn Ile Trp Asn Gln Phe Asn Trp Pro Phe
Gly Ala Leu Leu Cys Arg Val Ile Asn Gly Val Ile Lys Ala Asn
Leu Phe Ile Ser Ile Phe Leu Val Val Ala Ile Ser Gln Asp Arg
Tyr Arg Val Leu Val His Pro MET Ala Ser Gly Arg Gln Gln Arg
Arg Arg Gln Ala Arg Val Thr Cys Val Leu Ile Trp Val Val Gly
Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg Ser Ile Gln Ala
Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu Leu Pro His
Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile Leu Gly
Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His Ile
Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Cys
Gly Gly Arg Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu
Val Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala
Phe Leu Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe
Trp Glu Asp Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe
Ala Phe Thr Asn Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val
Gly Arg Leu Phe Arg Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys
Thr Pro Lys Ser Leu Ala Pro Ile Ser Ser Ser His Arg Lys Glu
Ile Phe Gln Leu Phe Trp Arg Asn SEQ.ID.NO.:2.

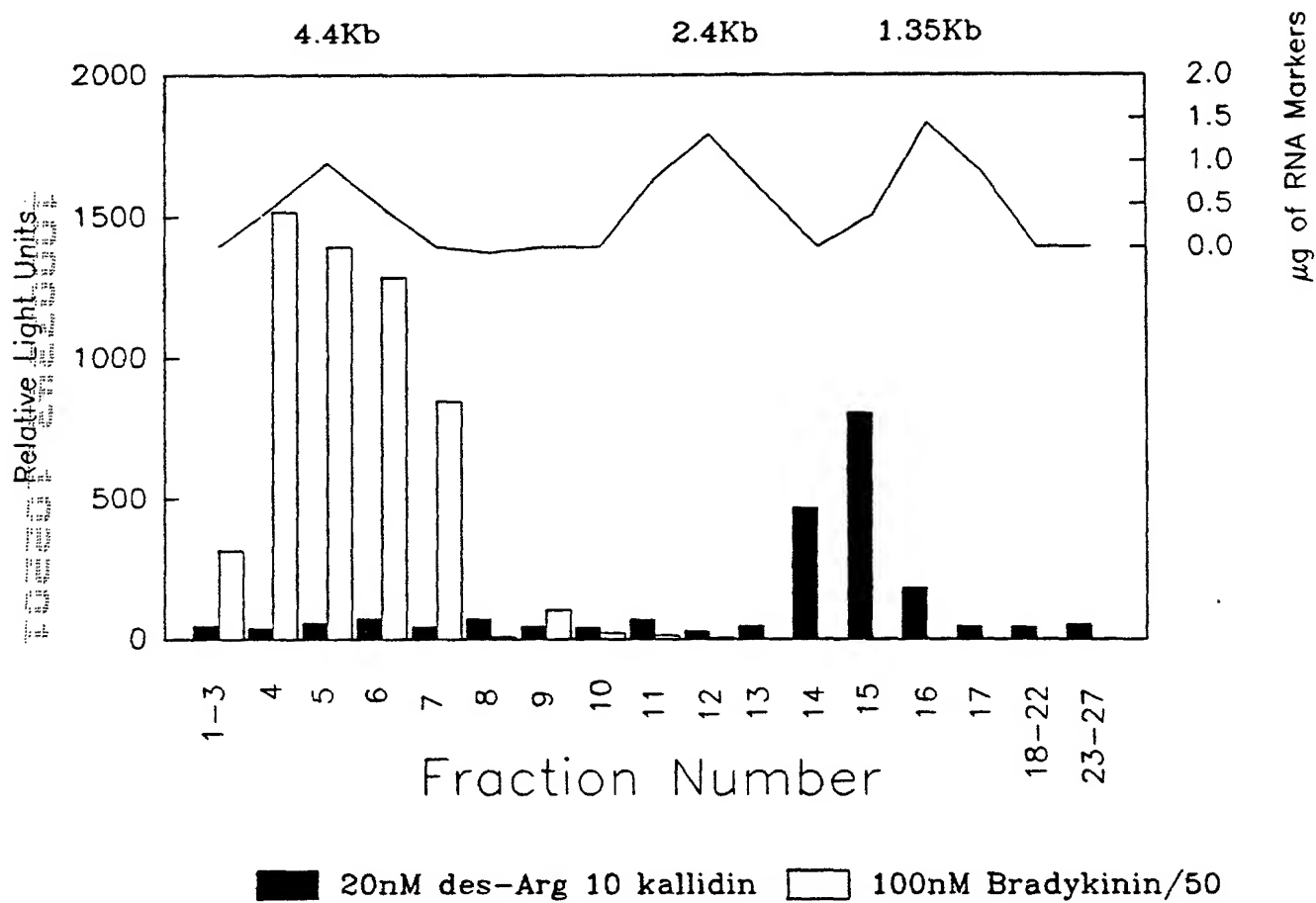


FIGURE 3

100
 50
 0
 10⁻¹³ 10⁻¹¹ 10⁻⁹ 10⁻⁷ 10⁻⁵
 Concentration (M)

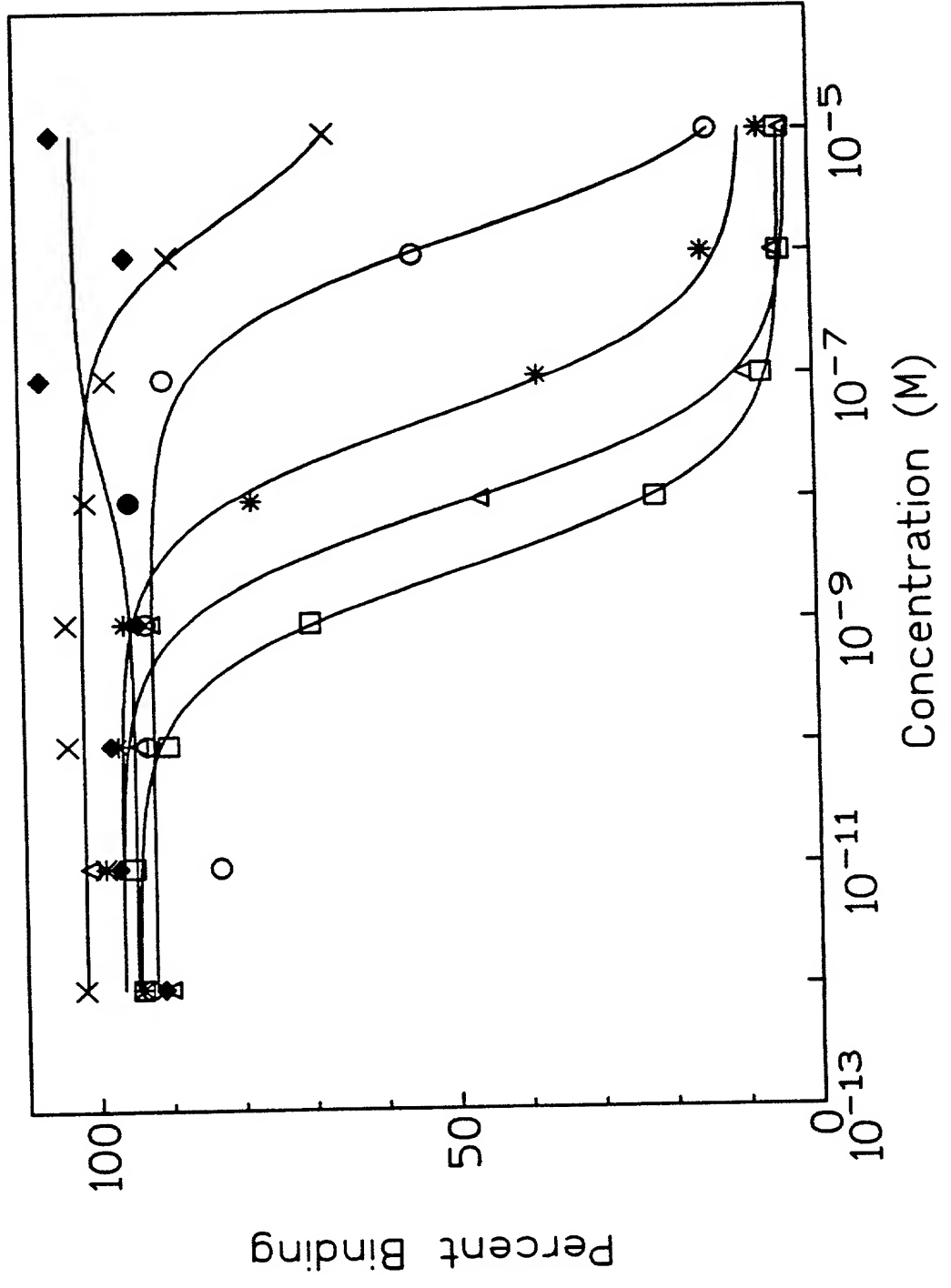


FIGURE 5